IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: **Ruben** *et al.*

Application Serial No.: 09/774,639 Art Unit: 1634

Filed: February 1, 2001 Examiner: Myers, C.

For: Secreted Protein HBJFE12 (as amended) Attorney Docket No.: PZ013P1C1

Commissioner for Patents
Washington, D.C. 20231

Declaration of Dr. George Komatsoulis Under 37 C.F.R. § 1.132

I, George Komatsoulis, do hereby declare and say:

1. I am a citizen of the United States, residing at 9518 Garwood Street, Silver Spring, MD, 20901.

2. Since February 3, 1997, I have served as a scientist of Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, Maryland 20850, assignee of the captioned application.

3. I have personal knowledge that the expression of the polynucleotide of SEQ ID NO:43 was assessed in hundreds of human tissues, including cancerous tissue (*e.g.*, B-cell lymphoma tissue), as well as many other "normal" (*i.e.*, non-cancerous) blood cells (*e.g.*, T cells, B cells, monocytes). Based on this assessment, no expression was observed in "normal" blood cells. In contrast, expression was observed in B-cell lymphoma tissue.

4. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the

United States code and that such willful false statements may jeopardize the validity of the application of any patents issued thereupon.

George J. Komatsoulis

Dr. George Komatsoulis

10 Jan - 2003

Date

☐ **1:** AC004804. Homo sapiens 12p1...[gi:3406032]


```
LOCUS       AC004804               108879 bp    DNA     linear   PRI 16-SEP-1998
DEFINITION  Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer
            Institute Human PAC library) complete sequence.
ACCESSION   AC004804
VERSION     AC004804.1  GI:3406032
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 108879)
  AUTHORS   Muzny,D., Arenson,A.D., Adams,C., Bunac,C., Carvelli,K., Chang,J.,
            Chacko,J., Chen,J., Ding,Y., Dugan,S., Durbin,J., Forcum,J.,
            Ganesh,R., Garcia,C., Goodman,M., Gorrell,J.H., Haywood,M.,
            Hernandez,J., Jackson,L., Jin,S., Kampal,R., Karpathy,S., Kovar,C.,
            Lau,S., Leal,B., Lee,E., Li,Y., Lichtarge,O., Liu,W., Logan,O.,
            Lu,J., Ly,T., Marondel,I., Martinez,C., Merscher,S., Montgomery,K.,
            Oswal,G., Perez,L., Rashid,N.D., Renault,B., Rowland,K., Savage,L.,
            Scherer,S.E., Shen,H., Simon,M., Stovall,K., Timms,K.M., Todd,J.,
            Vo,Q., Williamson,A., Worley,K.C., Yu,W., Kucherlapati,R.,
            Nelson,D. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 108879)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-1998) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 108879)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUL-1998) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   4  (bases 1 to 108879)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-1998) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   5  (bases 1 to 108879)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-1998) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   6  (bases 1 to 108879)
```

AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Aug 8, 1998 this sequence version replaced gi:3298526.
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.

The repeat regions shown were identified using RepeatMasker by Adrian Smit.

Sequence similarities were identified using Powerblast by Jinghui Zhang.

Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.

FEATURES	Location/Qualifiers
source	1..108879
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="12"
	/map="12p13.3"
	/clone="PAC RPCI5-927J10"
	/clone_lib="Roswell Park Cancer Institute Human PAC library"
repeat_region	complement(9..1193)
	/rpt_family="L1M4"
repeat_region	complement(1195..1495)
	/rpt_family="AluSx"
repeat_region	complement(1513..1607)
	/rpt_family="L1M4"
repeat_region	complement(1645..1827)
	/rpt_family="AluJo"
repeat_region	complement(2026..2335)
	/rpt_family="AluJb"
repeat_region	complement(2336..3054)
	/rpt_family="L1M4"
repeat_region	3056..3344
	/rpt_family="AluSp"
repeat_region	complement(3415..3616)
	/rpt_family="AluJo"
repeat_region	complement(3648..3843)
	/rpt_family="L1M4"
misc_feature	join(3745..4284,5658..6005)
	/note="Region: Similar to Unigene cluster 12346"
repeat_region	complement(4625..4720)
	/rpt_family="MIR"
repeat_region	complement(6110..6282)
	/rpt_family="AluSp"
repeat_region	complement(6285..6582)
	/rpt_family="AluY"
repeat_region	complement(6595..6890)
	/rpt_family="AluSg"
repeat_region	complement(6894..7026)
	/rpt_family="AluSq/x"

```
repeat_region   complement(7329..7356)
                /rpt_family="AT_rich"
repeat_region   7538..7567
                /rpt_family="AT_rich"
repeat_region   9287..9383
                /rpt_family="L1MC4"
repeat_region   complement(10492..10584)
                /rpt_family="(TA)n"
repeat_region   complement(10622..10670)
                /rpt_family="(CA)n"
repeat_region   11341..11471
                /rpt_family="AluSq/x"
repeat_region   complement(11720..11805)
                /rpt_family="L1M4"
repeat_region   complement(11874..12397)
                /rpt_family="MLT2CB"
repeat_region   complement(12452..12816)
                /rpt_family="L1M4"
repeat_region   complement(12871..12985)
                /rpt_family="L1M4"
repeat_region   complement(13094..13441)
                /rpt_family="L1M4"
repeat_region   complement(13442..13720)
                /rpt_family="AluSx"
repeat_region   complement(13753..14389)
                /rpt_family="L1M4"
misc_feature    join(14003..14230,14316..14601)
                /note="102882 gnl|UG|Hs#S102882 yf45h07.s2 Homo sapiens
                cDNA, 3' end clone=129853 R17017 770627 Hs.22099 and
                102919 gnl|UG|Hs#S102919 yf45h07.r2 Homo sapiens cDNA, 5'
                end clone=129853 gb=R17054 gi=770664 ug=Hs.22099; Region:
                102882 and 102919"
STS             14350..14478
                /standard_name="G24041"
                /note="WI-17199, Chr. 12, Homo sapiens"
                /db_xref="dbSTS:37879"
repeat_region   14661..14825
                /rpt_family="L1MC2"
repeat_region   14827..15066
                /rpt_family="AluJo"
repeat_region   15087..15988
                /rpt_family="L1MA3"
repeat_region   17058..17089
                /rpt_family="(CATA)n"
repeat_region   complement(17309..17529)
                /rpt_family="MIR"
repeat_region   complement(18983..19056)
                /rpt_family="(CA)n"
misc_feature    19447..19759
                /note="Region: AA663846 ae70b03.s1 Stratagene schizo brain
                S11 Homo sap iens cDNA clone 969485 3', mRNA sequence"
repeat_region   19762..20068
                /rpt_family="AluYb8"
repeat_region   complement(20069..20096)
                /rpt_family="AT_rich"
repeat_region   complement(22984..23190)
                /rpt_family="L2"
repeat_region   23217..23519
                /rpt_family="AluSx"
repeat_region   23886..24051
```

```
                     /rpt_family="MSTB"
repeat_region        24079..24202
                     /rpt_family="L2"
repeat_region        complement(24307..24549)
                     /rpt_family="AluSx"
repeat_region        24552..24723
                     /rpt_family="L2"
repeat_region        24966..25262
                     /rpt_family="AluSg"
repeat_region        25264..25294
                     /rpt_family="(TAAAA)n"
repeat_region        25296..25499
                     /rpt_family="L2"
repeat_region        complement(25929..26035)
                     /rpt_family="(TGGA)n"
repeat_region        complement(26054..26249)
                     /rpt_family="MER3"
repeat_region        complement(26358..26536)
                     /rpt_family="L1MC4"
repeat_region        complement(26788..27087)
                     /rpt_family="AluSg"
repeat_region        complement(27498..27720)
                     /rpt_family="MIR"
repeat_region        complement(27886..28056)
                     /rpt_family="L2"
repeat_region        28081..28204
                     /rpt_family="FAM"
repeat_region        28263..28471
                     /rpt_family="L2"
repeat_region        complement(28645..29247)
                     /rpt_family="CHARLIE2"
repeat_region        29248..29547
                     /rpt_family="AluSx"
repeat_region        complement(29548..29786)
                     /rpt_family="CHARLIE2"
repeat_region        complement(29811..29893)
                     /rpt_family="CHARLIE2"
repeat_region        30089..30234
                     /rpt_family="L2"
repeat_region        30361..30462
                     /rpt_family="L2"
repeat_region        complement(30970..31144)
                     /rpt_family="AluY"
repeat_region        complement(31976..32279)
                     /rpt_family="AluJo"
repeat_region        32303..32335
                     /rpt_family="AT_rich"
repeat_region        33051..33352
                     /rpt_family="AluSx"
repeat_region        complement(33375..33395)
                     /rpt_family="AT_rich"
repeat_region        33589..34338
                     /rpt_family="L1MC2"
misc_feature         complement(34817..35083)
                     /note="Region: T05792 EST03681 Fetal brain, Stratagene
                     (cat#936206) Homo s apiens cDNA clone HFBDG46, mRNA
                     sequence"
repeat_region        complement(35075..35374)
                     /rpt_family="AluY"
repeat_region        35766..36070
```

```
                     /rpt_family="AluSq"
repeat_region        38061..38097
                     /rpt_family="(CAAAA)n"
repeat_region        39934..40233
                     /rpt_family="AluSg"
repeat_region        41707..42005
                     /rpt_family="MER33"
repeat_region        complement(42318..42807)
                     /rpt_family="MLT1F"
repeat_region        43534..43831
                     /rpt_family="L1PA2"
repeat_region        43832..44124
                     /rpt_family="AluY"
repeat_region        44130..44802
                     /rpt_family="L1PA2"
repeat_region        44963..45244
                     /rpt_family="AluSx"
repeat_region        45245..45269
                     /rpt_family="AT_rich"
repeat_region        45283..45320
                     /rpt_family="MADE1"
repeat_region        complement(46066..46359)
                     /rpt_family="AluSp"
repeat_region        47530..47767
                     /rpt_family="L1MA4"
repeat_region        complement(49175..49212)
                     /rpt_family="AT_rich"
repeat_region        49718..50071
                     /rpt_family="MLT1A1"
repeat_region        50588..50858
                     /rpt_family="AluJo"
repeat_region        50859..50882
                     /rpt_family="AT_rich"
repeat_region        50912..50998
                     /rpt_family="L2"
repeat_region        51033..51200
                     /rpt_family="L2"
repeat_region        51279..51558
                     /rpt_family="L2"
repeat_region        complement(51740..52040)
                     /rpt_family="AluSp"
repeat_region        complement(52275..52481)
                     /rpt_family="L1MD3"
repeat_region        complement(52509..52772)
                     /rpt_family="AluJo"
repeat_region        complement(52806..53434)
                     /rpt_family="L1MC4"
repeat_region        complement(53439..53634)
                     /rpt_family="L1P4"
repeat_region        53685..53821
                     /rpt_family="FLAM_C"
repeat_region        53822..53886
                     /rpt_family="CHARLIE1"
repeat_region        54301..54444
                     /rpt_family="L1ME2"
repeat_region        54458..54533
                     /rpt_family="(GAAAA)n"
repeat_region        54937..55235
                     /rpt_family="AluSx"
repeat_region        55236..55257
```

```
                     /rpt_family="(CAAA)n"
repeat_region        complement(55932..56130)
                     /rpt_family="MER20"
repeat_region        56391..56537
                     /rpt_family="MER2"
repeat_region        complement(56542..56849)
                     /rpt_family="AluYb8"
repeat_region        56852..56914
                     /rpt_family="MER2"
repeat_region        57622..57900
                     /rpt_family="AluSx"
misc_feature         57873..57880
                     /note="Region: low coverage"
repeat_region        58570..58625
                     /rpt_family="L1P4"
repeat_region        complement(58972..59035)
                     /rpt_family="AT_rich"
repeat_region        complement(59617..59748)
                     /rpt_family="L1MC4"
repeat_region        59755..59940
                     /rpt_family="MER5A"
repeat_region        complement(59946..60017)
                     /rpt_family="L1MC4"
repeat_region        complement(60018..60308)
                     /rpt_family="AluJo"
repeat_region        60400..60645
                     /rpt_family="AluJo"
repeat_region        60879..60930
                     /rpt_family="AT_rich"
repeat_region        62028..62192
                     /rpt_family="MIR"
repeat_region        62405..62501
                     /rpt_family="(GAAA)n"
repeat_region        complement(63807..64365)
                     /rpt_family="L1ME"
repeat_region        complement(64382..64668)
                     /rpt_family="AluJb"
repeat_region        complement(65209..65303)
                     /rpt_family="L1M4"
repeat_region        65308..65403
                     /rpt_family="MER47B"
repeat_region        65402..65592
                     /rpt_family="MER47B"
misc_feature         complement(65670..66004)
                     /note="Region: AA324338 EST27143 Cerebellum II Homo
                     sapiens cDNA 5' end , mRNA sequence"
repeat_region        complement(66265..66566)
                     /rpt_family="AluSx"
repeat_region        66832..66864
                     /rpt_family="AT_rich"
repeat_region        66893..67716
                     /rpt_family="L1MA"
repeat_region        67718..68007
                     /rpt_family="AluY"
repeat_region        68082..69454
                     /rpt_family="L1MA9"
repeat_region        69457..69750
                     /rpt_family="AluSx"
repeat_region        69752..70224
                     /rpt_family="L1MA9"
```

```
repeat_region   complement(70250..70512)
                /rpt_family="AluJo"
repeat_region   70530..72778
                /rpt_family="L1MA9"
repeat_region   72779..73078
                /rpt_family="AluSx"
repeat_region   73086..73485
                /rpt_family="L1MA9"
STS             74097..74337
                /standard_name="Z51010"
                /note="AFM142xc7, Chr. 12, Homo sapiens"
                /db_xref="dbSTS:28930"
repeat_region   complement(74262..74305)
                /rpt_family="(CA)n"
repeat_region   complement(74308..74564)
                /rpt_family="AluJo"
repeat_region   complement(74757..75056)
                /rpt_family="AluJo"
repeat_region   75113..75140
                /rpt_family="AT_rich"
repeat_region   complement(75468..75507)
                /rpt_family="(CA)n"
repeat_region   76213..76309
                /rpt_family="MER5A"
repeat_region   76650..76715
                /rpt_family="L2"
repeat_region   77241..77530
                /rpt_family="AluSx"
repeat_region   complement(77568..77882)
                /rpt_family="MER7A"
repeat_region   complement(78526..78882)
                /rpt_family="L2"
repeat_region   79024..79133
                /rpt_family="MER58B"
repeat_region   complement(79358..79858)
                /rpt_family="L2"
repeat_region   79879..80119
                /rpt_family="AluJb"
repeat_region   complement(80260..80463)
                /rpt_family="L2"
repeat_region   80583..80877
                /rpt_family="AluSx"
repeat_region   complement(80886..80935)
                /rpt_family="(TA)n"
repeat_region   complement(80961..82137)
                /rpt_family="L2"
misc_feature    complement(82757..83095)
                /note="Region: AA324430 EST27251 Cerebellum II Homo
                sapiens cDNA 5' end , mRNA sequence"
repeat_region   84174..84207
                /rpt_family="AT_rich"
repeat_region   84789..85022
                /rpt_family="MIR"
repeat_region   complement(85050..85147)
                /rpt_family="(CA)n"
repeat_region   complement(85834..85997)
                /rpt_family="AluSg/x"
repeat_region   complement(86000..86300)
                /rpt_family="AluSx"
repeat_region   86880..87216
```

```
                     /rpt_family="MER61"
repeat_region        87886..88194
                     /rpt_family="AluSq"
repeat_region        88308..88593
                     /rpt_family="AluSp"
repeat_region        complement(88756..89041)
                     /rpt_family="AluSc"
repeat_region        89984..90137
                     /rpt_family="MER5A"
repeat_region        90503..90788
                     /rpt_family="AluSx"
repeat_region        90793..90974
                     /rpt_family="AluSq"
repeat_region        91290..91514
                     /rpt_family="MER30"
repeat_region        91553..91729
                     /rpt_family="MIR"
repeat_region        complement(91791..91899)
                     /rpt_family="MER53"
repeat_region        complement(92745..92874)
                     /rpt_family="MER85"
repeat_region        complement(93396..93431)
                     /rpt_family="MIR"
repeat_region        complement(94317..94395)
                     /rpt_family="(TA)n"
repeat_region        94563..94734
                     /rpt_family="MIR"
repeat_region        96398..96693
                     /rpt_family="AluSx"
repeat_region        complement(97009..97031)
                     /rpt_family="AT_rich"
repeat_region        complement(97082..97378)
                     /rpt_family="AluJb"
repeat_region        complement(98726..98813)
                     /rpt_family="(TA)n"
repeat_region        98898..99196
                     /rpt_family="AluY"
misc_feature         99820..99856
                     /note="Region: low coverage"
repeat_region        complement(99956..100266)
                     /rpt_family="AluSq"
repeat_region        100422..100527
                     /rpt_family="MSTA"
repeat_region        100527..100614
                     /rpt_family="MSTA"
repeat_region        100614..100701
                     /rpt_family="MSTA"
repeat_region        100698..100795
                     /rpt_family="MSTC"
repeat_region        100788..101167
                     /rpt_family="MSTA"
repeat_region        101528..101827
                     /rpt_family="AluJb"
repeat_region        101828..101870
                     /rpt_family="(CAAAA)n"
repeat_region        102475..102776
                     /rpt_family="AluSx"
repeat_region        complement(102779..102849)
                     /rpt_family="(CA)n"
repeat_region        102850..102953
```

```
                     /rpt_family="(GA)n"
     repeat_region   102968..103257
                     /rpt_family="AluJb"
     repeat_region   104428..104642
                     /rpt_family="L1ME2"
     repeat_region   complement(105315..105617)
                     /rpt_family="AluSx"
     repeat_region   105817..106187
                     /rpt_family="MLT2E"
     repeat_region   complement(106211..106325)
                     /rpt_family="(CATA)n"
     repeat_region   107733..107770
                     /rpt_family="MIR"
     misc_feature    107916..108123
                     /note="Region: AA149367 zo29f12.s1 Stratagene colon
                     (#937204) Homo sapi ens cDNA clone 588335 3',"
     misc_feature    108534..108879
                     /note="Bases 1-347 in AC004804 overlap."
                     /function="Overlap with adjacent clone AC004802"
BASE COUNT    36381 a  20956 c  19880 g  31662 t
ORIGIN
        1 ggatccattt ggtagggacc tatcaatttt tttttaattc tttaaagaac ccggttatga
       61 attttgtgaa ttttctgttg attctctgtc ttctatgtgt ttgatttctg ttatctttaa
      121 tatttccgtt atcctactta ctgtggttta ctctgcttct ttttctggta ccttagtgta
      181 gaaactaaga tcaatgaatt tcaacttttc ttcttttcta atacaggtat ataagggtaa
      241 aaatttcatt ctaaccactt tttcaactgt gaaacacaaa acttcacatt tgaattttca
      301 ttcagttcaa aacgagtcct aacattcctt cttctctaag ccatggtatt tagaattatg
      361 ttatctaatt tccaaacatt ttctaagtat cttattaact tctaactgaa ttctactgtg
      421 gttagagaac aactttagca tatctcagtc ttctgaaatt tactgagact tacttttaag
      481 gcccagcata tggtctgtat ctgtgaaact tccatatgca cttaaaaaac atatattttc
      541 ttcagttgtt agatgtagta ttctataaat gttaaataag tcaagttaat agtctttaga
      601 tcttctatat ttctgattgc ttttgtttgt ttagtaattc tatcagtttc taaggaatag
      661 aggtcaaaat ccccagtaat gactggtgac cacagatttg ttttaccttt agttctgtcg
      721 gtctgtcctt catgaatttt gaagctctat tagatatata tttattagga ttattatgtc
      781 atttggatgt gttgtcccct ttatctttat tatatggtct tttcttatct ctgggaatac
      841 tctttgtctg atattaatat agctatgcca ggtttcttag gattactatt tccaagaagt
      901 acctttttcc gttaattcca gccagtgttt atgatagtac aggtcttatg tacagcatac
      961 agttgagcct tgctttttt tttctaatct agtatctctg tcctttactt ggtgtgttta
     1021 ctatatttca ttttgccata aatattgata tggttgaatt tatgtcattc atttgttgtt
     1081 tctgttcttt atttgttgtt ccttttctgc ctttattggt tggataaatg aaacaatttt
     1141 tagcattgca ttttatttcc tctgttagct cttcaggtgc tttttctttg tttgtttgtt
     1201 ttttttttt ttgtgacaga gtctcgttct gtcgtccagg ctggagtgca gtggcgccat
     1261 cttggctcac tgcaacctct gcctcccagg ttcaagcaat tctcctgcct cagaatcccg
     1321 agtagctggg ataacagaca cccgccacca cacccggcta gtttttgtat ttttagtaga
     1381 gatgggggtt tcaccacgtt ggccaagctg gtctcaaact cctgacctca agtgatccgt
     1441 gcgccttggg ctcccaaagt gctgggatta caggcctgag ccatggtgcc tggccgctct
     1501 tcagggtttt taaaattttt gttgttatta ttttggtagt tgctctacag ctaacaacat
     1561 gcaccttatc aaagtctatt tagattagaa attgtactac ttcacatcga acacttcgta
     1621 atctatcttt ctttctctct ttcctttctt ctttttttg ttagagacca ggttttactc
     1681 tgtcaaccat gctagtgtgc agtggcacaa acagaactca gtgtaaactc aaaatcctgg
     1741 gctcaagtga tcctccagtc tcagcttccc aaagcactgg gatcacaggc atgagtcacc
     1801 atgcccagcc aacagttcat attttctact tcacgaacgt aagaacctta caattctacc
     1861 tcctaatatt ttgggatact gttgtcccat ctttcacttt tacacatatt ataaatgcca
     1921 actcatcatg ttatttttgc tttaaatggt tagttgtctt ttaagggaat tctgagaaga
     1981 aaaaatacat tttctatatg tatcaactga tttaccatgt ctgtgttttt ttttttttt
     2041 ttggcagggg gacagagtct cactctatca cccaggctgg agtgcagtgg tgtgatcttg
     2101 gcttactaca gcctccgtgt cctgggccca ggaatcctca gtctcagcct cccaagtaat
     2161 tggaacaaga gtatgagcca ccatcctcag ctaatttttt ttttttttt ttttttgtag
     2221 aaacagggtt tcgtcatgtt gtctaggctg gtctcagact cctggactca agtgatcctc
     2281 ccaccttggc ctctcaaagc gttgagatta caggcatgag ccacagtgcc cggcccatgt
```

2341 ctggtgttct tcattccttc ctgtagattc atgctcccat ctggattcat ttcccttcag
2401 cttgaagaac actcattagc atttcttcta gagtgctttc tagagatgaa ttcttttcat
2461 atttgtttat atgaaattgt ctttatttaa tcctagtttt taaaggatct ttttctttgc
2521 ttacagaatt ttaggctaat tttttttttt ttttttagta ccctgaaaga agttccattg
2581 tcttcaggtc ctcactgttt ctgataagga ctcagctatc atagtttccc tttatgcact
2641 gtgccttttt tcttaggctg cttttatttt tctctgcata ttttgtttcc agcaactgga
2701 ctatggtatt tctagttgtg attttttttat tttttgtatt tatcctgctt ggtttcactt
2761 agtttctggg atttgtaaat caaagattca tggtttcaaa ttaaattata gaaatatgtt
2821 ggccattttt aaaaactgtc tttcatctgc ttcattctca ctcttttatc cttctagtgt
2881 tccacatgta tgttaaccca tttgaaattg tcctacatgt cactgaggct ctgttcattc
2941 ggtaaaaatc ctttcactcc ctgttctaca gattgaataa tttcaattga tctattttga
3001 agttcactga ctctttcttt tgacagctct aattttccat taagactatc caataggctg
3061 ggcacggtgg ctgacgcctg taatcccagc actttgggag gccaacctga ggttgggagt
3121 ttgagaccag cctgaccaac atggaaaaac ctcgcctcta ctaaaaatac aaaattagct
3181 ggctgtgatg gcgcatgcct gtaatcccag ctactcggga ggctgaggca ggaggatcgc
3241 ctgaacccag gaggcggagg ttgcagtgag ccgagatggc gccactgcac tccagcctgg
3301 gggacaagag cgacactcca tctcaaaaaa aaaaaaaaaa aaaaaaaaaa aaagactatc
3361 caataaatgt ttcatttcta tttcaattat caaatttcca ttttcatttt atgattatta
3421 ctttttgag atagggtctc attttgttgc ccaggccgga gtatgctggc acaatcaaag
3481 ttcactgcag cctcaatctc ccaggctcaa gcaatcctct cacctcaccc tcccaagtag
3541 ttgggactat aggtgtgcac caccacacct ggctggtatt taaaaacatt tttgtagaga
3601 caggttctca ctatgtcaaa tttccatttt aaaatacttt tcctttctct gttgagattt
3661 cctatctatt ccatcatcaa catgacattt ttctttaatt ctttaatgta taagggtgaa
3721 tttagttgtt ttttttttt ttttctgtta aaccaaatag gactcctcag aggtgatttc
3781 tactgcatgc tcttttctgc tctatagatc atatgttcct gattctttgc atgtctggta
3841 attaaaagtt caacatggga tatattgcaa atatggttct gttaatttct tctgaggagc
3901 agtgattttt attctagtac atataagtca gttaatagtt gactccttga acttgtatag
3961 gtttggattt aacctttggt atgctgatct gctgaaagct caggatattt cccaggcttc
4021 tctatctcgg tgagactcat tgtccaaatt tggtctaccc tgtaagaatt aattggggcc
4081 ttcttttact agtcttagcc tgggtctaga gtaggcctta tattagagca tggtccttgt
4141 tcctcaaacc tatcttttgt gttatctcag ctagataact gaagttaaca aggatttctc
4201 catgttgact gggttggaac tccagattcc ccacggctct atctctaata ttacaattcc
4261 actctcattc tgtagcatct aatctctggt aagccttggg cagtctcatt cagtgaacac
4321 gtagcctagt cctcagccag gaatcatgat acctggcttc caacttctcc tcagtatact
4381 gtgcttgtat atgaattact tccctgattt acacaggaca tttacaacta cagaatcagg
4441 ggacctcagg aggtcatctg gccaaagtcc acaattttta aatcgatggg ggacctttcg
4501 aatctgagtg agaaaactgc agacctgaaa agctaagtga tttctccagg tacgaacaca
4561 aaagcacaaa ttggattttc agttgtaaat gtcatgcttt gcaagcacat tcagctttac
4621 caacttcaac gtgctttttt aaaatctcat ttgatccgta caacaacttc atgaggtggg
4681 tctaagtctt actatgcctg cttcacgggt aagcaaactg gcccaaaatg taagcaaatc
4741 ctttgctaca cagaccatct tctaatcctc tttcattcag taacttctgg aagaaaagct
4801 tatgattaaa tggatagatt actatctttg acatccatag cttgagggga gttttaccta
4861 tttggagagt gagtagctac ctataaggta cactctggag aacaatgaaa aagatggtcc
4921 tgaaaggaaa attaaaaaac aaaaaacatc aaaaatccaa acaaaaccaa aaaaacctgc
4981 catactggta aattatatat cagattttct tcaactgggt attgcaatta ggttaacgca
5041 tcaggttacc tacctacaat aattaacctt ttaaatgatt catttatatt taacaaaagg
5101 gatgagggtt gatcctatac ctccaacaga gaaaaaaaga aaagataagg aaaaagtagg
5161 acaataatct cacttccttc cttttgtgag gagtagatga cagacagtct taatttcatc
5221 cctacacagg taagcacatt tttacacgtg aaccatatat tgatagagag agagaaagaa
5281 ttttgaaagc tgaaaacaag agggactttc ggagccttta tctgaaaagt ttagttcttt
5341 atttgttact tagaccttat tccagccact tgaggctttt tacataagaa aatgattaaa
5401 aagcatggat tttttttttaa acatggtttc ttctatttgg aagttatgtc tgatcttaaa
5461 aagctaaaat gtggaataag tttaaaattt aaagaaggag aaaggcaaag aacatttagg
5521 gttatttgta atttattcca attcatgtca caagaaagta aagaaatgtc tatagggtgg
5581 gccgtataaa agcactgaat atcagggcag aaaaaaggga agcagaatga gagagttaag
5641 caaaactgag gaggagtccc aagggatagt tgattgtaga tataaacttt gcttcataat
5701 tttaactagt cccagaccca ccaatgctat ttgtttatag ctatactgta caacatattg
5761 ttttcttttt caagtgtaaa ataatttttat attatgtggg tttcctacat aacattcaac
5821 ctcagtattc tagcccattg tgaaaaatgc ttccaagtcc actaaaagtc ctttatcata
5881 tgtctacaga cttaaaaaaa atggcttttg gtggaagtat aaataaatat ggctttgtga

```
>AC004804 /chromosome="12" /map="12p13.3" Homo sapiens 12p13.3 PAC RPCI5-927J10
          (Roswell Park Cancer Institute Human PAC library) complete sequence.
          Length = 108,879

  Plus Strand HSPs:

 Score = 3170 (481.7 bits), Expect = 3.3e-143, Sum P(2) = 3.3e-143
 Identities = 650/661 (98%), Positives = 650/661 (98%), Strand = Plus / Plus

Gene33:    70 GCAATCTCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAATAAATAAATAAAA 129
              ||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20012 GCAGTC-CGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAATAAATAAATAAAA 20070

Gene33:   130 TAAAATTAAATTAAAAAAAAAAAAAAAAAGTCTGCTTTGAAAACCAGTATCCATAGACTT 189
              |||||| |||||||||||||||||||   |||||||||||||||||||||||||||||
Sbjct: 20071 TAAAATAAAATTAAAAAAAAAAAAAA---GTCTGCTTTGAAAACCAGTATCCATAGACTT 20127

Gene33:   190 CTGGCAGTCATTTCTGGGGTTTAATTTTGGATGTGACAAAGGTTTGTTTCCACTGGACTT 249
              ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct: 20128 CTGGCAGTCATTTCTGGGGTTTAATTTTGGATGTGCCAAAGGTTTGTTTCCACTGGACTT 20187

Gene33:   250 AATTTTTTCACATCGCTCTAACTTTTGAAAACACAGATACAGTCCTTTTGCTGAATAAAA 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20188 AATTTTTTCACATCGCTCTAACTTTTGAAAACACAGATACAGTCCTTTTGCTGAATAAAA 20247

Gene33:   310 TGAAAACTCGAGCCTAAATTTAAAGGCATAGATATTTCCTGGACTTCCAGGACAGTAATA 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20248 TGAAAACTCGAGCCTAAATTTAAAGGCATAGATATTTCCTGGACTTCCAGGACAGTAATA 20307

Gene33:   370 TCATGTACTACTTTGTCAAAAAAATTTTCTGGAGGTTTTTCTAGAGGAAGAAACTAAGAT 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20308 TCATGTACTACTTTGTCAAAAAAATTTTCTGGAGGTTTTTCTAGAGGAAGAAACTAAGAT 20367

Gene33:   430 AACAACAACAAAAAA-GACAAATCCAAATGCATTACTTGAAGAGCGACTACTCATGTTTC 488
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20368 AACAACAACAAAAAAAGACAAATCCAAATGCATTACTTGAAGAGCGACTACTCATGTTTC 20427

Gene33:   489 TAGAGAATTTTTTTGGTCATACTATGTCATGGGGTTATTTCCTGGGGGGCTTCAGTTCTGCT 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20428 TAGAGAATTTTTTTGGTCATACTATGTCATGGGGTTATTTCCTGGGGGGCTTCAGTTCTGCT 20487

Gene33:   549 TCAGAATTTCTTTAGTAGTTATCTACTGACCCCATCTGGTAAAATTATAGAGGAAGTTAC 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20488 TCAGAATTTCTTTAGTAGTTATCTACTGACCCCATCTGGTAAAATTATAGAGGAAGTTAC 20547

Gene33:   609 AGTCGTTAAAGCTTCTGTCAACTCGATTTCTAAAAATTTTATGTAAAGAGATATTTTAAG 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 20548 AGTCGTTAAAGCTTCTGTCAACTCGATTTCTAAAAATTTTATGTAAAGAGATATTTTAAG 20607

Gene33:   669 AGAAATAAGAAAATAGGAGATCAGGGCAAATGAATCTAAAGATCTTTAGCTTTACTCGTG 728
              |||||||||||||||||||||||||||||||||||||||||||||||||||| || |
Sbjct: 20608 AGAAATAAGAAAATAGGAGATCAGGGCAAATGAATCTAAAGATCTTTAGCTTTA-TCTTC 20666

Gene33:   729 C 729
              |
Sbjct: 20667 C 20667
```

1: Hematol Pathol 1991;5(1):21-6 Related Articles, Links

Loss of genetic material from the short arm of chromosome 12 is a frequent secondary abnormality in non-Hodgkin's lymphoma.

Jonveaux P, Le Coniat M, Derre J, Vecchione D, Berger R.

Unite INSERM U 301, Institut de Genetique Moleculaire, Paris, France.

Abnormalities of the short arm of chromosome 12 have been detected in a wide variety of hematopoietic disorders. Seven cases of non-Hodgkin's lymphoma (NHL) are reported with various rearrangements involving bands 12p13 or 12p11, associated with other chromosome changes. A review of the literature confirms that rearrangements of 12p, mainly at band 12p13, are nonrandom chromosomal abnormalities in all subtypes of NHL, as in other malignant blood disorders. No common translocation could, however, be detected, and 12p abnormalities may be considered as secondary chromosomal events. Most of the 12p rearrangements involving translocation of genetic material of unknown origin, suggest that they result in loss of 12p segment.

PMID: 2050601 [PubMed - indexed for MEDLINE]

1: Genes Chromosomes Cancer 1997 Oct;20(2):155-66

FISH identifies different types of duplications with 12q13-15 as the commonly involved segment in B-cell lymphoproliferative malignancies characterized by partial trisomy 12.

Dierlamm J, Wlodarska I, Michaux L, Vermeesch JR, Meeus P, Stul M, Criel A, Verhoef G, Thomas J, Delannoy A, Louwagie A, Cassiman JJ, Mecucci C, Hagemeijer A, Van den Berghe H.

Center for Human Genetics, University of Leuven, Belgium.

Clinical, cytogenetic, fluorescence in situ hybridization (FISH), and Southern blot data of 18 patients with different subtypes of B-cell non-Hodgkin's lymphoma, cytogenetically characterized by partial trisomy 12, are presented. These chromosomal changes occurred predominantly in clinically progressive chronic lymphocytic leukemia, mixed cell type, and advanced-stage follicle center cell lymphoma at the time of relapse or transformation into diffuse large cell lymphoma. Partial trisomy 12 consistently included the long arm of chromosome 12, either completely or partially, and resulted from dup(12q) or other rearrangements involving chromosome 12. The duplications were cytogenetically identified as dup(12)(q13q23), dup(12)(q13q22), or dup(12)(q13q15) in follicle center cell lymphoma or t(14;18)-positive diffuse large cell lymphoma; dup(12)(q13q22) or dup(12)(q13q24) in chronic lymphocytic leukemia; and dup(12)(q13q21) in a case of t(14;18)-negative diffuse large cell lymphoma. FISH, using library probes and a panel of YAC probes, mapped along the long arm of chromosome 12, confirmed the cytogenetic results in all cases analyzed except for three cases of t(14;18)-positive follicle center lymphoma or diffuse large cell lymphoma with dup(12q). In these cases, FISH showed similar, possibly identical, duplications, which involved a region more centromeric (12q11-21) than assumed by karyotypic analysis (12q13-22 or 12q13-23) and included alphoid DNA sequences, a combination hitherto unknown. In addition, commonly duplicated regions of chromosome 12 could be defined: 12q11-21, including alphoid DNA sequences for follicle center cell lymphoma or t(14;18)-positive diffuse large cell lymphoma, 12q13-22 for chronic lymphocytic leukemia, and 12p13-q15 for marginal zone cell lymphoma, all of which overlapped in 12q13-15. Whether these regions, especially 12q13-15, may contain genes which are important in

malignant transformation or disease progression of B-cell lymphoproliferative malignancies characterized by complete or partial trisomy 12 remains to be determined.

PMID: 9331566 [PubMed - indexed for MEDLINE]
